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7148.003 Sequence Listing.ST25  
SEQUENCE LISTING

<110> Cummings, Richard D.

Ju, Tongzhong

<120> CORE1 BETA-3 GALACTOSYLTRANSFERASE SPECIFIC MOLECULAR CHAPARONES, NUCLEIC ACIDS, AND METHODS OF USE THEREOF

<130> 7148.003

<150> 60/411,310

<151> 2002-09-13

<160> 16

<170> PatentIn version 3.1

<210> 1

<211> 318

<212> PRT

<213> Homo sapiens

<400> 1

Met Leu Ser Glu Ser Ser Ser Phe Leu Lys Gly Val Met Leu Gly Ser  
1 5 10 15

Ile Phe Cys Ala Leu Ile Thr Met Leu Gly His Ile Arg Ile Gly His  
20 25 30

Gly Asn Arg Met His His His Glu His His His Leu Gln Ala Pro Asn  
35 40 45

Lys Glu Asp Ile Leu Lys Ile Ser Glu Asp Glu Arg Met Glu Leu Ser  
50 55 60

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Lys Ser Phe Arg Val Tyr Cys Ile Ile Leu Val Lys Pro Lys Asp Val  
65 70 75 80

Ser Leu Trp Ala Ala Val Lys Glu Thr Trp Thr Lys His Cys Asp Lys  
85 90 95

Ala Glu Phe Phe Ser Ser Glu Asn Val Lys Val Phe Glu Ser Ile Asn  
100 105 110

Met Asp Thr Asn Asp Met Trp Leu Met Met Arg Lys Ala Tyr Lys Tyr  
115 120 125

Ala Phe Asp Lys Tyr Arg Asp Gln Tyr Asn Trp Phe Phe Leu Ala Arg  
130 135 140

Pro Thr Thr Phe Ala Ile Ile Glu Asn Leu Lys Tyr Phe Leu Leu Lys  
145 150 155 160

Lys Asp Pro Ser Gln Pro Phe Tyr Leu Gly His Thr Ile Lys Ser Gly  
165 170 175

Asp Leu Glu Tyr Val Gly Met Glu Gly Ile Val Leu Ser Val Glu  
180 185 190

Ser Met Lys Arg Leu Asn Ser Leu Leu Asn Ile Pro Glu Lys Cys Pro  
195 200 205

Glu Gln Gly Gly Met Ile Trp Lys Ile Ser Glu Asp Lys Gln Leu Ala  
210 215 220

Val Cys Leu Lys Tyr Ala Gly Val Phe Ala Glu Asn Ala Glu Asp Ala  
225 230 235 240

Asp Gly Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Ser Ile Lys  
245 250 255

Glu Ala Met Thr Tyr His Pro Asn Gln Val Val Glu Gly Cys Cys Ser  
260 265 270

Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln Met His Val  
275 280 285

Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly His Ile Phe Asn

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290

295

300

Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser Asp Asn Asp  
305 310 315

&lt;210&gt; 2

&lt;211&gt; 957

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<400> 2  
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catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga ggatgagcgc 180  
atggagctca gtaaagagctt tcgagtatac tgtatttatcc ttgtaaaacc caaagatgtg 240  
agtctttggg ctgcagtaaa ggagacttgg accaaacact gtgacaaagc agagttcttc 300  
agttctgaaa atgttaaagt gtttgagtca attaatatgg acacaaatga catgtggta 360  
atgatgagaa aagcttacaa atacgcctt gataagtata gagaccaata caactggttc 420  
ttccttgcac gccccactac gtttgctatc attgaaaacc taaagtattt tttgtaaaa 480  
aaggatccat cacagcctt ctagcttaggc cacactataa aatctggaga cttgaatat 540  
gtgggtatgg aaggaggaat tgtcttaagt gttagaatcaa tgaaaagact taacagcctt 600  
ctcaatatcc cagaaaagtg tcctgaacag ggagggatga tttggaagat atctgaagat 660  
aaacagctag cagttgcct gaaatatgct ggagtattt cagaaaatgc agaagatgct 720  
gatggaaaag atgtatttaa taccaaattt gttggcttt ctattaaaga ggcaatgact 780  
tatcacccca accaggttgtt agaaggctgt tgttcagata tggctgttac tttatgg 840  
ctgactccaa atcagatgca tgtgatgatg tatgggtat accgccttag ggcatttggg 900  
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&lt;210&gt; 3

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

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<400> 3

Met Leu Ser Glu Ser Ser Ser Phe Leu Lys Gly Val Met Leu Gly Ser  
1 5 10 15

Ile Phe Cys Ala Leu Ile Thr Met Leu Gly His Ile Arg Ile Gly Asn  
20 25 30

Arg Met His His His Glu His His His Leu Gln Ala Pro Asn Lys Asp  
35 40 45

Asp Ile Ser Lys Ile Ser Glu Ala Glu Arg Met Glu Leu Ser Lys Ser  
50 55 60

Phe Arg Val Tyr Cys Ile Val Leu Val Lys Pro Lys Asp Val Ser Leu  
65 70 75 80

Trp Ala Ala Val Lys Glu Thr Trp Thr Lys His Cys Asp Lys Ala Glu  
85 90 95

Phe Phe Ser Ser Glu Asn Val Lys Val Phe Glu Ser Ile Asn Met Asp  
100 105 110

Thr Asn Asp Met Trp Leu Met Met Arg Lys Ala Tyr Lys Tyr Ala Tyr  
115 120 125

Asp Gln Tyr Arg Asp Gln Tyr Asn Trp Phe Phe Leu Ala Arg Pro Thr  
130 135 140

Thr Phe Ala Val Ile Glu Asn Leu Lys Tyr Phe Leu Leu Lys Lys Asp  
145 150 155 160

Gln Ser Gln Pro Phe Tyr Leu Gly His Thr Val Lys Ser Gly Asp Leu  
165 170 175

Glu Tyr Val Ser Val Asp Gly Gly Ile Val Leu Ser Ile Glu Ser Met  
180 185 190

Lys Arg Leu Asn Ser Leu Leu Ser Val Pro Glu Lys Cys Pro Glu Gln  
195 200 205

Gly Gly Met Ile Trp Lys Ile Ser Glu Asp Lys Gln Leu Ala Val Cys  
210 215 220

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Leu Lys Tyr Ala Gly Val Phe Ala Glu Asn Ala Glu Asp Ala Asp Gly  
225 230 235 240

Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Phe Ile Lys Glu Ala  
245 250 255

Met Thr Asn Gln Pro Asn Gln Val Val Glu Gly Cys Cys Ser Asp Met  
260 265 270

Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln Met His Val Met Met  
275 280 285

Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly His Val Phe Asn Asp Ala  
290 295 300

Leu Val Phe Leu Pro Pro Asn Gly Ser Glu Asn Asp  
305 310 315

<210> 4

<211> 1432

<212> DNA

<213> Mus musculus

<400> 4  
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gtgatgctg gaagcatctt ctgtgcctt atcaactatgc taggccacat taggattgga 180  
aacagaatgc accaccatga gcatcaccat ctgcaagccc ctaacaaaga cgatatctcg 240  
aaaatttcag aggctgaacg catggagctc agtaagagtt tccgggtata ctgtatagtt 300  
cttgtaaaac ccaaagatgt gagtcttgg gctgcagtga aggagactt gaccaaacac 360  
tgtgacaaaag cagaattctt cagttctgaa aatgttaaag tgtttgagtc aatataatg 420  
gacacaaaatg acatgtgggtt gatgatgagg aaagcttaca aatatgctta tgatcaatac 480  
agggaccaat acaactgggtt cttccttgca cgccccacta ctttcgtgt tattgaaaac 540  
ctcaaataatt ttttgttaaa aaaggatcaa tcccaacctt tctatctcgg acacactgta 600  
aaatctggag accttgaata tgtgagtgtg gatggaggaa ttgtcttaag catagaatca 660  
atgaaaagac tcaacagtct tctcagtgtt cctgaaaagt gtcctgaaca aggaggaatg 720

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atttggaaga tatctgaaga taaacagctg gcggctcgcc tgaaatacgc cggagtattt	780
gcagaaaatg ccgaagatgc cgatggaaaa gatgtgttta ataccaaatac cgttggcctt	840
ttcattaaag aggcaatgac taaccaacca aaccaggtag tagaaggctg ttgctctgat	900
atggctgtta cttaaatgg actgactcct aatcagatgc acgtgatgat gtatgggtg	960
taccggctta gggcatttgg acatgtttc aatgatgcat tggtttctt acctccaaat	1020
ggttctgaga atgactgaca gaaagcaaga gcatgcattt agtaactata ttacgacatg	1080
gtatcatttt taattgatga cagatctaac atagtaatat gattctttt ctatcttt	1140
acccattgaa gtctgcttgt acaatgtcaa atggaatgct gttttccct tataatcattc	1200
ctgagaaatt aaaatgtatt aaaaataaat gtttaaaaaa tagcaatttt tcaaacacat	1260
atttataagt atatttatgt gataaagact aaattataga cattgtaatc tgtggtgtat	1320
ctttgcttat tggttttaaa cttatgtatc attttagctt tgtaatataat gtaaatgaga	1380
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<210> 5

<211> 313

<212> PRT

<213> Brachydanio rerio

<400> 5

Met Met Ser Glu Gly Ser Ser Phe Met Lys Gly Met Ile Leu Gly Gly			
1	5	10	15

Ile Phe Cys Leu Ile Met Ser Phe Phe Glu Thr Phe Asn Pro Gly Thr		
20	25	30

His Ser Glu Gly His Asn His Leu His His Leu Lys Pro Val Ser		
35	40	45

Lys Asp Glu Leu Gln Lys Leu Ser Glu Ser Gln Met Ser Glu Phe Ala		
50	55	60

Met Gln Val Arg Val Tyr Cys Leu Ile Met Val Thr Pro Lys Leu Leu			
65	70	75	80

Val His Trp Ala Thr Ala Asn Asp Thr Trp Ser Lys His Cys Asp Lys

Ser Val Phe Tyr Thr Ser Glu Ala Ser Lys Ala Leu Asp Ala Val Asp  
100 105 110

Leu Gln Glu Gln Asp Glu Trp Thr Arg Leu Arg Lys Ala Ile Gln His  
115 120 125

Ala Tyr Glu Asn Ala Gly Asp Leu His Trp Phe Phe Ile Ala Arg Pro  
130 135 140

Thr Thr Phe Ala Ile Glu Asn Leu Lys Tyr Leu Val Leu Asp Lys  
145 150 155 160

Asp Pro Ser Gln Pro Phe Tyr Ile Gly His Thr Glu Lys Ser Gly Glu  
165 170 175

Leu Asp Tyr Val Glu Tyr Asp Ser Gly Ile Val Leu Ser Tyr Glu Ala  
180 185 190

Met Arg Arg Leu Met Glu Val Phe Lys Asp Glu Asp Lys Cys Pro Glu  
195 200 205

Arg Gly Arg Ala Leu Trp Lys Met Ser Glu Glu Lys Gln Leu Ala Thr  
210 215 220

Cys Leu Lys Tyr Ser Gly Val Phe Ala Glu Asn Gly Glu Asp Ala Gln  
225 230 235 240

Gly Lys Gly Leu Phe Asn Lys Lys Ser Val Ser Ser Leu Ile Ser Asp  
245 250 255

Ser Ile Ser Gln Asn Pro Gly Asp Val Val Glu Ala Cys Cys Ser Asp  
260 265 270

Met Ala Ile Thr Phe Ala Gly Met Ser Pro Ser Gln Ile Gln Val Leu  
275 280 285

Met Tyr Gly Val Tyr Arg Leu Arg Pro Tyr Gly His Asp Phe His Asp  
290 295 300

Ser Leu Thr Phe Leu Pro Pro Arg Leu  
305 310

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&lt;210&gt; 6

&lt;211&gt; 1223

&lt;212&gt; DNA

&lt;213&gt; Brachydanio rerio

&lt;400&gt; 6

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gttcgagtct	actgcctcat	catggtcaact	ccaaagcttt	tagttcaactg	ggcgacagct	300
aacgacacct	ggagcaaaca	ctgcgacaaa	tctgtgtttt	acacctctga	ggcgtctaaa	360
gctctagatg	cgggtgaccc	acaggagcag	gacgagtgga	caaggcttcg	caaagccatc	420
caacacgctt	atgagaacgc	cgagacactg	cactggtttt	tcatagcgcg	acccaccacc	480
tttgcattata	tagagaatct	caaatacctg	gtgttgata	aagatccaag	ccagccgttt	540
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gtgttgagtt	atgaagcgat	gaggaggctg	atggaggtgt	ttaaagatga	agataaatgt	660
ccagagcgag	gacgagctct	atggaagatg	tctgaagaaa	agcaactggc	cacttgtctg	720
aagtacagcg	gagtgtttgc	tgaaaacgga	gaggacgccc	aaggcaaagg	gcttttaac	780
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actgtgactc	tcagcagtga	aatgttgatc	ataattgggt	gcgggatgaa	ttatttgtga	1080
agttggtgaa	ggtaaaaaatg	aaaatgattt	gcattatgtat	ttaataactaa	taagtcaagt	1140
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&lt;210&gt; 7

&lt;211&gt; 316

&lt;212&gt; PRT

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<213> Rattus norvegicus

<400> 7

Met Leu Ser Glu Ser Ser Ser Phe Leu Lys Gly Val Met Leu Gly Ser  
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Ile Phe Cys Ala Leu Ile Thr Met Leu Gly His Ile Arg Ile Gly Asn  
20 25 30

Arg Met His His His Glu His His His Leu Gln Ala Pro Asn Lys Asp  
35 40 45

Asp Ile Leu Lys Ile Ser Glu Thr Glu Arg Met Glu Leu Ser Lys Ser  
50 55 60

Phe Gln Val Tyr Cys Ile Val Leu Val Lys Pro Lys Asp Val Ser Leu  
65 70 75 80

Trp Ala Ala Val Lys Glu Thr Trp Thr Lys His Cys Asp Lys Ala Glu  
85 90 95

Phe Phe Ser Ser Glu Asn Val Lys Val Phe Glu Ser Ile Asn Met Asp  
100 105 110

Thr Asn Asp Met Trp Leu Met Met Arg Lys Ala Tyr Lys Tyr Ala Tyr  
115 120 125

Asp Lys Tyr Lys Asp Gln Tyr Asn Trp Phe Phe Leu Ala Arg Pro Thr  
130 135 140

Thr Phe Ala Val Ile Glu Asn Leu Lys Tyr Phe Leu Leu Arg Lys Asp  
145 150 155 160

Pro Ser Gln Pro Phe Tyr Leu Gly His Thr Val Lys Ser Gly Asp Leu  
165 170 175

Glu Tyr Val Ser Val Asp Gly Gly Ile Val Leu Ser Ile Glu Ser Met  
180 185 190

Lys Arg Leu Asn Gly Leu Leu Ser Val Pro Glu Lys Cys Pro Glu Gln  
195 200 205

7148.003 Sequence Listing.ST25  
Gly Gly Met Ile Trp Lys Ile Ser Glu Asp Lys Gln Leu Ala Val Cys  
210 215 220

Leu Lys Tyr Ala Gly Val Phe Ala Glu Asn Ala Glu Asp Ala Asp Gly  
225 230 235 240

Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Phe Ile Lys Glu Ala  
245 250 255

Met Thr Asn Gln Pro Asn Gln Val Val Glu Gly Cys Cys Ser Asp Met  
260 265 270

Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln Met His Val Met Met  
275 280 285

Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly His Val Phe Asn Asp Ala  
290 295 300

Leu Val Phe Leu Pro Pro Asn Gly Ser Glu Asn Asp  
305 310 315

<210> 8

<211> 1283

<212> DNA

<213> Rattus norvegicus

<400> 8  
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gtatactgta tagttctcgta aaaacctaaa gatgtgagtc tttgggctgc agtgaaggag 180  
acttggacca aacactgtga caaaggcagaa ttcttcagtt ctgaaaatgt taaagtgttt 240  
gagtcaattha atatggacac aaatgatatg tggttgatga tgaggaaagc ttacaaatat 300  
gcttatgata aatacaagga ccaataaac tggttcttcc ttgcacgccc cactacttc 360  
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ctaggtcaca ctgtaaaatc tggagacctt gaatatgtga gtgtggatgg aggaattgtc 480  
ttaaggcatag aatcaatgaa aagactcaat ggccttctca gtgtccctga aaagtgtcct 540  
gaacaaggag gaatgatttg gaagatatct gaagataagc agctagcagt ctgcctgaaa 600

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tttttcttat ctggttacac tggtaataatc acacattgaa gtctacttgt acattgtcaa	1020
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tttggtcctt acctccgagg gaa	1283

<210> 9

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Completely synthesized.

<400> 9

ctccatagag gagttgttgc

20

<210> 10

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Completely synthesized.

<400> 10

tcacgcctttt ctaccacttc

20

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<210> 11

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Completely synthesized.

<400> 11

gcggatccat ggcctctaaa tc 22

<210> 12

<211> 69

<212> DNA

<213> Artificial sequence

<220>

<223> Completely synthesized.

<400> 12

ggaagatcta cttgccgtcg atcagcctgg ggtccacctg gtcctcagga tttcctaact 60

tcacttttg 69

<210> 13

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> Completely synthesized.

<400> 13

Glu Asp Gln Val Asp Pro Arg Leu Ile Asp Gly Lys  
1 5 10

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<210> 14

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> Completely synthesized.

<400> 14

Ala Ser Lys Ser Trp Leu Asn Phe Leu  
1 5

<210> 15

<211> 18

<212> PRT

<213> Artificial sequence

<220>

<223> Completely synthesized.

<400> 15

Met Leu Ser Glu Ser Ser Ser Phe Leu Lys Gly Val Met Leu Gly Ser  
1 5 10 15

Ile Phe

<210> 16

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> Completely synthesized.

<400> 16

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His His His Glu His His His  
1 5